

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/820,745

DATE: 11/26/2001

TIME: 12:34:34

Input Set : A:\620-139.app  
 Output Set: N:\CRF3\11212001\I820745.raw

P5  
ENTERED

3 <110> APPLICANT: Blundell, Tom L  
 4       Abell, Christopher  
 5       Inoue, Tsuyoshi  
 6       von Delft, Frank  
 8 <120> TITLE OF INVENTION: Crystal Structure  
 10 <130> FILE REFERENCE: 620-139  
 12 <140> CURRENT APPLICATION NUMBER: US 09/820,745  
 13 <141> CURRENT FILING DATE: 2001-03-30  
 15 <160> NUMBER OF SEQ ID NOS: 12  
 17 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 8  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Artificial Sequence  
 24 <220> FEATURE:  
 25 <223> OTHER INFORMATION: Description of Artificial Sequence: Conserved  
 26       sequence motif  
 28 <400> SEQUENCE: 1  
 29 Leu Val Gly Asp Ser Leu Gly Met  
 30       1                         5  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 6  
 35 <212> TYPE: PRT  
 36 <213> ORGANISM: Artificial Sequence  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: Description of Artificial Sequence: Conserved  
 40       sequence motif  
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 43 Val Lys Ile Glu Gly Gly  
 44       1                         5  
 47 <210> SEQ ID NO: 3  
 48 <211> LENGTH: 8  
 49 <212> TYPE: PRT  
 50 <213> ORGANISM: Artificial Sequence  
 52 <220> FEATURE:  
 53 <223> OTHER INFORMATION: Description of Artificial Sequence: Conserved  
 54       sequence motif  
 56 <220> FEATURE:  
 57 <221> NAME/KEY: SITE  
 58 <222> LOCATION: (3)  
 59 <223> OTHER INFORMATION: Xaa is a hydrophobic residue  
 61 <400> SEQUENCE: 3  
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 63       1                         5  
 66 <210> SEQ ID NO: 4  
 67 <211> LENGTH: 7  
 68 <212> TYPE: PRT

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69 <213> ORGANISM: Artificial Sequence  
71 <220> FEATURE:  
72 <223> OTHER INFORMATION: Description of Artificial Sequence: Conserved  
73 sequence motif  
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76 Gly Gly Tyr Lys Val Gln Gly  
77 1 5  
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81 <211> LENGTH: 6  
82 <212> TYPE: PRT  
83 <213> ORGANISM: Artificial Sequence  
85 <220> FEATURE:  
86 <223> OTHER INFORMATION: Description of Artificial Sequence: Conserved  
87 sequence motif  
89 <400> SEQUENCE: 5  
90 Ile Gly Ile Gly Ala Gly  
91 1 5  
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95 <211> LENGTH: 6  
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97 <213> ORGANISM: Artificial Sequence  
99 <220> FEATURE:  
100 <223> OTHER INFORMATION: Description of Artificial Sequence: Conserved  
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103 <400> SEQUENCE: 6  
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105 1 5  
108 <210> SEQ ID NO: 7  
109 <211> LENGTH: 264  
110 <212> TYPE: PRT  
111 <213> ORGANISM: Escherichia coli  
113 <400> SEQUENCE: 7  
114 Met Lys Pro Thr Thr Ile Ser Leu Leu Gln Lys Tyr Lys Gln Asp Lys  
115 1 5 10 15  
117 Lys Arg Phe Ala Thr Ile Thr Ala Tyr Asp Tyr Ser Phe Ala Lys Leu  
118 20 25 30  
120 Phe Ala Asp Glu Gly Leu Asn Val Met Leu Val Gly Asp Ser Leu Gly  
121 35 40 45  
123 Met Thr Val Gln Gly His Asp Ser Thr Leu Pro Val Thr Val Ala Asp  
124 50 55 60  
126 Ile Ala Tyr His Thr Ala Ala Val Arg Arg Gly Ala Pro Asn Cys Leu  
127 65 70 75 80  
129 Leu Leu Ala Asp Leu Pro Phe Met Ala Tyr Ala Thr Pro Glu Gln Ala  
130 85 90 95  
132 Phe Glu Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Met Val Lys  
133 100 105 110  
135 Ile Glu Gly Gly Glu Trp Leu Val Glu Thr Val Gln Met Leu Thr Glu  
136 115 120 125  
138 Arg Ala Val Pro Val Cys Gly His Leu Gly Leu Thr Pro Gln Ser Val

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139      130          135          140
141 Asn Ile Phe Gly Gly Tyr Lys Val Gln Gly Arg Gly Asp Glu Ala Gly
142 145          150          155          160
144 Asp Gln Leu Leu Ser Asp Ala Leu Ala Leu Glu Ala Ala Gly Ala Gln
145          165          170          175
147 Leu Leu Val Leu Glu Cys Val Pro Val Glu Leu Ala Lys Arg Ile Thr
148          180          185          190
150 Glu Ala Leu Ala Ile Pro Val Ile Gly Ile Gly Ala Gly Asn Val Thr
151          195          200          205
153 Asp Gly Gln Ile Leu Val Met His Asp Ala Phe Gly Ile Thr Gly Gly
154          210          215          220
156 His Ile Pro Lys Phe Ala Lys Asn Phe Leu Ala Glu Thr Gly Asp Ile
157 225          230          235          240
159 Arg Ala Ala Val Arg Gln Tyr Met Ala Glu Val Glu Ser Gly Val Tyr
160          245          250          255
162 Pro Gly Glu Glu His Ser Phe His
163          260
166 <210> SEQ ID NO: 8
167 <211> LENGTH: 267
168 <212> TYPE: PRT
169 <213> ORGANISM: Schizosaccharomyces pombe
171 <400> SEQUENCE: 8
172 Met Ser Leu Lys Gln Ile Thr Ile Ser Thr Leu Arg Gln Trp Lys Leu
173   1          5          10          15
175 Ala Asn Lys Lys Phe Ala Cys Ile Thr Ala Tyr Asp Ala Ser Phe Ser
176   20          25          30
178 Arg Leu Phe Ala Glu Gln Gly Met Pro Val Met Leu Val Gly Asp Ser
179   35          40          45
181 Leu Gly Met Thr Ala Gln Gly His Ser Thr Thr Leu Pro Val Ser Val
182   50          55          60
184 Glu Asp Ile Ala Tyr His Thr Lys Ser Val Arg Arg Gly Ala Pro Asn
185   65          70          75          80
187 Arg Leu Leu Met Ala Asp Leu Pro Phe Met Ser Tyr Ser Thr Trp Glu
188   85          90          95
190 Asp Ala Cys Lys Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Ile
191   100         105         110
193 Val Lys Ile Glu Gly Gly Asn Trp Ile Phe Glu Ile Val Gln Arg
194   115         120         125
196 Leu Thr Glu Arg Ser Val Pro Val Ala Gly His Leu Gly Leu Thr Pro
197   130         135         140
199 Gln Ser Val Asn Ile Phe Gly Gly Tyr Lys Ile Gln Gly Arg Glu Gln
200 145          150          155          160
202 Ser Ala Ala Ala Arg Leu Ile Glu Asn Ala Gln Gln Leu Glu Lys Phe
203          165          170          175
205 Gly Ala Gln Leu Leu Val Leu Glu Cys Ile Pro Glu Ser Leu Ala Glu
206          180          185          190
208 Gln Ile Thr Lys Thr Ile Ser Ile Pro Thr Ile Gly Ile Gly Ala Gly
209          195          200          205
211 Lys His Thr Asp Gly Gln Ile Leu Val Met His Asp Ala Leu Gly Ile

```

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Input Set : A:\620-139.app

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212 210 215 220  
 214 Thr Gly Gly Arg Pro Pro Lys Phe Ala Lys Asn Phe Leu Ser Gly Ala  
 215 225 230 235 240  
 217 Gly Asp Ile Arg Thr Ala Ile Gln Arg Tyr Ile Tyr Glu Val Glu Gln  
 218 245 250 255  
 220 Gly Leu Tyr Pro Ala Glu Glu His Ser Phe Gln  
 221 260 265  
 224 <210> SEQ ID NO: 9  
 225 <211> LENGTH: 349  
 226 <212> TYPE: PRT  
 227 <213> ORGANISM: Aspergillus nidulans  
 229 <400> SEQUENCE: 9  
 230 Met Thr Phe Leu Arg Ile Ala Thr Lys Arg Ala Ile Tyr Leu His Arg  
 231 1 5 10 15  
 233 Pro Ala Asn Pro Ala Leu Pro Thr Ser Ser Ile Leu Pro Val Leu His  
 234 20 25 30  
 236 Ser Thr Asn Val Ala Thr Arg Val Pro Ser Pro Cys Ala Ile Arg His  
 237 35 40 45  
 239 Ser Ser His Ser Pro Leu Gly Ala Ala Gln Ala Asn Pro Arg Lys Lys  
 240 50 55 60  
 242 Val Thr Met Gln Thr Leu Arg Asn Leu Tyr Lys Lys Gly Glu Pro Ile  
 243 65 70 75 80  
 245 Thr Met Leu Thr Ala His Asp Phe Pro Ser Ala His Val Ala Asp Ala  
 246 85 90 95  
 248 Ala Gly Met Asp Met Ile Leu Val Gly Asp Ser Leu Ala Met Val Ala  
 249 100 105 110  
 251 Leu Gly Met Gln Asp Thr Ser Glu Val Thr Leu Asp Asp Met Leu Val  
 252 115 120 125  
 254 His Cys Arg Ser Val Ala Arg Ala Ala Gln Ser Ala Phe Thr Val Ser  
 255 130 135 140  
 257 Asp Leu Pro Met Gly Ser Tyr Glu Val Ser Pro Glu Gln Ala Leu Gln  
 258 145 150 155 160  
 260 Ser Ala Ile Arg Ile Val Lys Glu Gly Arg Val Gln Gly Val Lys Leu  
 261 165 170 175  
 263 Glu Gly Glu Glu Met Ala Pro Ala Ile Lys Arg Ile Thr Thr Ala  
 264 180 185 190  
 266 Gly Ile Pro Val Val Gly His Ile Gly Leu Thr Pro Gln Arg Gln Asn  
 267 195 200 205  
 269 Ala Leu Gly Gly Phe Arg Val Gln Gly Lys Ser Thr Thr Asp Ala Leu  
 270 210 215 220  
 272 Lys Leu Leu Lys Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Met  
 273 225 230 235 240  
 275 Ile Val Ile Glu Ala Val Pro Pro Glu Ile Ala Ser Ile Val Thr Gln  
 276 245 250 255  
 278 Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Cys Ser  
 279 260 265 270  
 281 Gly Gln Val Leu Val Gln Ile Asp Met Thr Gly Asn Phe Pro Pro Gly  
 282 275 280 285  
 284 Arg Phe Leu Pro Lys Phe Val Lys Gln Tyr Ala Asn Val Trp Asn Glu

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285	290	295	300													
287	Ala	Leu	Gln	Gly	Ile	Gln	Gln	Tyr	Arg	Glu	Glu	Val	Lys	Ser	Arg	Ala
288	305				310			315								320
290	Tyr	Pro	Ala	Glu	Gln	His	Thr	Tyr	Pro	Ile	Pro	Lys	Glu	Glu	Leu	Val
291						325				330						335
293	Glu	Phe	Gln	Lys	Ala	Val	Asp	Glu	Leu	Pro	Glu	Glu	Lys			
294						340			345							
297	<210>	SEQ ID NO:	10													
298	<211>	LENGTH:	347													
299	<212>	TYPE:	PRT													
300	<213>	ORGANISM:	Arabidopsis thaliana													
302	<400>	SEQUENCE:	10													
303	Met	Ala	Ser	Ser	Leu	Thr	Arg	Asn	Cys	Ser	Arg	Phe	Ser	Lys	Ala	Ile
304	1				5					10						15
306	Ser	Val	Arg	Phe	Met	Ser	Asn	Leu	Pro	Glu	Asn	Thr	Val	Tyr	Gly	Gly
307						20				25						30
309	Pro	Lys	Pro	Gln	Asn	Pro	Asn	Gln	Arg	Val	Thr	Leu	Thr	His	Leu	Arg
310						35			40							45
312	Gln	Lys	His	Arg	Arg	Gly	Glu	Pro	Ile	Thr	Val	Val	Thr	Ala	Tyr	Asp
313						50			55							60
315	Tyr	Pro	Ser	Ala	Val	His	Leu	Asp	Thr	Ala	Gly	Ile	Asp	Val	Cys	Leu
316						65			70			75				80
318	Val	Gly	Asp	Ser	Ala	Ser	Met	Val	Val	His	Gly	His	Asp	Thr	Thr	Leu
319						85				90						95
321	Pro	Ile	Ser	Leu	Asp	Glu	Met	Leu	Val	His	Cys	Arg	Ala	Val	Ala	Arg
322						100			105							110
324	Gly	Ala	Lys	Arg	Pro	Leu	Leu	Val	Gly	Asp	Leu	Pro	Phe	Gly	Thr	Tyr
325						115			120							125
327	Glu	Ser	Ser	Ser	Gln	Ala	Val	Asp	Thr	Ala	Val	Arg	Val	Leu	Lys	
328						130			135			140				
330	Glu	Gly	Gly	Met	Asp	Ala	Ile	Lys	Leu	Glu	Gly	Gly	Ser	Ala	Ser	Arg
331						145			150			155				160
333	Ile	Thr	Ala	Ala	Lys	Ala	Ile	Val	Glu	Ala	Gly	Ile	Ala	Val	Ile	Gly
334						165				170						175
336	His	Val	Gly	Leu	Thr	Pro	Gln	Ala	Ile	Ser	Val	Leu	Gly	Gly	Phe	Arg
337						180			185							190
339	Pro	Gln	Gly	Arg	Asn	Ile	Ala	Ser	Ala	Val	Lys	Val	Val	Glu	Thr	Ala
340						195			200			205				
342	Met	Ala	Leu	Gln	Glu	Ala	Gly	Cys	Phe	Ser	Val	Val	Leu	Glu	Cys	Val
343						210			215			220				
345	Pro	Pro	Pro	Val	Ala	Ala	Ala	Ala	Thr	Ser	Ala	Leu	Lys	Ile	Pro	Thr
346						225			230			235				240
348	Ile	Gly	Ile	Gly	Ala	Gly	Pro	Phe	Cys	Ser	Gly	Gln	Val	Leu	Val	Tyr
349						245				250						255
351	His	Asp	Leu	Leu	Gly	Met	Met	Gln	His	Pro	His	His	Ala	Lys	Val	Thr
352						260			265			270				
354	Pro	Lys	Phe	Cys	Lys	Gln	Tyr	Ala	Asn	Val	Gly	Glu	Val	Ile	Asn	Lys
355						275			280			285				
357	Ala	Leu	Met	Glu	Tyr	Lys	Glu	Glu	Val	Ser	Lys	Lys	Val	Phe	Pro	Gly

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
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Input Set : A:\620-139.app  
Output Set: N:\CRF3\11212001\I820745.raw

L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12